



#8

# SEQUENCE LISTING

<110> Bolton, Alexandra J.  
Perez-Casal, Jose  
Fontaine, Michael  
Potter, Andrew A.

<120> IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST  
STREPTOCOCCUS INFECTION

<130> 9000-0055

<140> 09/878,781

<141> 2001-06-11

<160> 18

<170> PatentIn Ver. 2.0

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<213> Artificial Sequence

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<212> DNA

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<221> CDS

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Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp	
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Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro	
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Arg	Gly	Gly	Asp	Leu	Arg	Arg	Ala	Arg	Ala	Gly	Ala	Ala	Asn	Ile	Val	195	200	205	
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Tyr	Thr	Glu	Asp	Pro	Ile	Val	Ser	Ser	Asp	Ile	Val	Gly	Val	Ser	Tyr	275	280	285	
Gly	Ser	Leu	Phe	Asp	Ala	Thr	Gln	Thr	Lys	Val	Met	Glu	Val	Asp	Gly	290	295	300	
Ser	Gln	Leu	Val	Lys	Val	Val	Ser	Trp	Tyr	Asp	Asn	Glu	Met	Ser	Tyr	305	310	315	320
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gca ttc cgt cgc atc caa aac gta gaa ggt gtt gaa gtt act cgt atc	96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile	
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aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tat gac	144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp	
35 40 45	
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Thr Gly Phe Phe Ala Ser Lys Glu Lys Ala Gly Gln His Ile His Glu	
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Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
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Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val	
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Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
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Glu Glu Val Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly	
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Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr	
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Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly	
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Phe	Asp	Val	Asn	Gly	Lys	Phe	Ile	Lys	Val	Ser	Ala	Glu	Lys	Asp	Pro	
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gaa caa att gac tgg gca act gac ggt gtt gaa atc gtt ctt gaa gca															288	
Glu	Gln	Ile	Asp	Trp	Ala	Thr	Asp	Gly	Val	Glu	Ile	Val	Leu	Glu	Ala	
			85						90					95		
act ggt ttc ttt gct aaa aaa gca gct gct gaa aaa cat tta cat gaa															336	
Thr	Gly	Phe	Phe	Ala	Lys	Lys	Ala	Ala	Ala	Glu	Lys	His	Leu	His	Glu	
			100					105					110			
aat ggt gct aaa aaa gtt gtt atc act gct cct ggt gga gat gac gtg															384	
Asn	Gly	Ala	Lys	Lys	Val	Val	Ile	Thr	Ala	Pro	Gly	Gly	Asp	Asp	Val	
		115					120					125				
aaa aca gtt gta ttt aac act aac cat gat atc ctt gat gga act gaa															432	
Lys	Thr	Val	Val	Phe	Asn	Thr	Asn	His	Asp	Ile	Leu	Asp	Gly	Thr	Glu	
	130					135					140					
aca gtt att tca ggt gct tca tgt act aca aac tgt tta gct cca atg															480	
Thr	Val	Ile	Ser	Gly	Ala	Ser	Cys	Thr	Thr	Asn	Cys	Leu	Ala	Pro	Met	

145	150	155	160	
gct aaa gct tta caa gat aac ttt ggc gta aaa caa ggt tta atg act	528			
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr				
165 170 175				
aca atc cac gct tac act ggt gat caa atg ctt ctt gat gga cct cac	576			
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Leu Leu Asp Gly Pro His				
180 185 190				
cgt ggt ggt gac tta cgt cgt gcc cgt gct ggt gct aac aat att gtt	624			
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Asn Asn Ile Val				
195 200 205				
cct aac tca act ggt gct gct aaa gca atc ggt ctt gtt atc cct gaa	672			
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu				
210 215 220				
tta aat ggt aaa ctt gac ggt gct gca caa cgt gta cca gtt cca aca	720			
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr				
225 230 235 240				
ggt tca gta aca gaa tta gta gca gtt ctt aat aaa gaa act tca gta	768			
Gly Ser Val Thr Glu Leu Val Ala Val Leu Asn Lys Glu Thr Ser Val				
245 250 255				
gaa gaa att aac tca gta atg aaa gct gca gct aat gat tca tat ggt	816			
Glu Glu Ile Asn Ser Val Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly				
260 265 270				
tac act gaa gat cca atc gta tca tct gat atc gtt ggt atg tct ttc	864			
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Phe				
275 280 285				
ggt tca tta ttc gat gct act caa act aaa gta caa act gtt gat gga	912			
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly				
290 295 300				
aat caa tta gtt aaa gtt gtt tca tgg tat gac aat gaa atg tct tac	960			
Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr				
305 310 315 320				
act gct caa ctt gat cgt aca ctt gag tac ttt gca aaa atc gct aaa	1008			
Thr Ala Gln Leu Asp Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys				
325 330 335				
taa	1011			

<210> 10  
 <211> 336  
 <212> PRT  
 <213> Streptococcus parauberis

<400> 10

Met	Val	Val	Lys	Val	Gly	Ile	Asn	Gly	Phe	Gly	Arg	Ile	Gly	Arg	Leu
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Ala	Phe	Arg	Arg	Ile	Gln	Asn	Val	Glu	Gly	Val	Glu	Val	Thr	Arg	Ile
			20					25					30		
Asn	Asp	Leu	Thr	Asp	Pro	Asn	Met	Leu	Ala	His	Leu	Leu	Lys	Tyr	Asp
		35					40					45			
Thr	Thr	Gln	Gly	Arg	Phe	Asp	Gly	Thr	Val	Glu	Val	Lys	Asp	Gly	Gly
	50					55					60				
Phe	Asp	Val	Asn	Gly	Lys	Phe	Ile	Lys	Val	Ser	Ala	Glu	Lys	Asp	Pro
65					70					75					80
Glu	Gln	Ile	Asp	Trp	Ala	Thr	Asp	Gly	Val	Glu	Ile	Val	Leu	Glu	Ala
			85						90					95	
Thr	Gly	Phe	Phe	Ala	Lys	Lys	Ala	Ala	Ala	Glu	Lys	His	Leu	His	Glu
			100					105					110		
Asn	Gly	Ala	Lys	Lys	Val	Val	Ile	Thr	Ala	Pro	Gly	Gly	Asp	Asp	Val
		115					120					125			
Lys	Thr	Val	Val	Phe	Asn	Thr	Asn	His	Asp	Ile	Leu	Asp	Gly	Thr	Glu
	130					135					140				
Thr	Val	Ile	Ser	Gly	Ala	Ser	Cys	Thr	Thr	Asn	Cys	Leu	Ala	Pro	Met
145					150					155				160	
Ala	Lys	Ala	Leu	Gln	Asp	Asn	Phe	Gly	Val	Lys	Gln	Gly	Leu	Met	Thr
			165						170					175	
Thr	Ile	His	Ala	Tyr	Thr	Gly	Asp	Gln	Met	Leu	Leu	Asp	Gly	Pro	His
		180						185					190		
Arg	Gly	Gly	Asp	Leu	Arg	Arg	Ala	Arg	Ala	Gly	Ala	Asn	Asn	Ile	Val
		195					200					205			
Pro	Asn	Ser	Thr	Gly	Ala	Ala	Lys	Ala	Ile	Gly	Leu	Val	Ile	Pro	Glu
	210					215					220				
Leu	Asn	Gly	Lys	Leu	Asp	Gly	Ala	Ala	Gln	Arg	Val	Pro	Val	Pro	Thr
225					230				235					240	
Gly	Ser	Val	Thr	Glu	Leu	Val	Ala	Val	Leu	Asn	Lys	Glu	Thr	Ser	Val
			245						250					255	
Glu	Glu	Ile	Asn	Ser	Val	Met	Lys	Ala	Ala	Ala	Asn	Asp	Ser	Tyr	Gly
			260					265				270			
Tyr	Thr	Glu	Asp	Pro	Ile	Val	Ser	Ser	Asp	Ile	Val	Gly	Met	Ser	Phe
		275					280					285			

Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly  
 290 295 300

Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr  
 305 310 315 320

Thr Ala Gln Leu Asp Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys  
 325 330 335

<210> 11

<211> 1011

<212> DNA

<213> Streptococcus iniae

<220>

<221> CDS

<222> (1)..(1011)

<400> 11

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 Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu  
 1 5 10 15

gca ttc cgt cgt att caa aat gtt gaa ggt gtt gaa gta act cgt atc 96  
 Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile  
 20 25 30

aat gac ctt aca gat cct aac atg ctt gca cac ttg ttg aaa tat gat 144  
 Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp  
 35 40 45

aca act caa ggt cgt ttt gac ggt aca gtt gaa gtt aaa gat ggt gga 192  
 Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly  
 50 55 60

ttc gaa gtt aac gga agc ttt gtt aaa gtt tct gca gaa cgc gaa cca 240  
 Phe Glu Val Asn Gly Ser Phe Val Lys Val Ser Ala Glu Arg Glu Pro  
 65 70 75 80

gca aac att gac tgg gct act gat ggt gta gac atc gtt ctt gaa gca 288  
 Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Asp Ile Val Leu Glu Ala  
 85 90 95

aca ggt ttc ttc gct tct aaa gca gct gct gaa caa cac att cac gct 336  
 Thr Gly Phe Phe Ala Ser Lys Ala Ala Ala Glu Gln His Ile His Ala  
 100 105 110

aac ggt gcg aaa aaa gtt gtt atc aca gct cct ggt gga aat gac gtt 384  
 Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val  
 115 120 125

aaa aca gtt gtt tac aac act aac cat gat att ctt gat gga act gaa 432  
 Lys Thr Val Val Tyr Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu

130	135	140	
aca gtt atc tca ggt gct tca tgt act	aca aac tgt tta gct cca atg	480	
Thr Val Ile Ser Gly Ala Ser Cys Thr	Thr Asn Cys Leu Ala Pro Met		
145	150 155 160		
gct aaa gca tta caa gat aac ttt ggt gta aaa caa ggt tta atg act	528		
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr			
165 170 175			
act atc cat ggt tac act ggt gac caa atg gtt ctt gac gga cca cac	576		
Thr Ile His Gly Tyr Thr Gly Asp Gln Met Val Leu Asp Gly Pro His			
180 185 190			
cgt ggt ggt gat ctt cgt cgt gct cgt gca gct gca gca aac atc gtt	624		
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Ala Ala Asn Ile Val			
195 200 205			
cct aac tca act ggt gct gct aaa gca atc ggt ctt gtt atc cca gaa	672		
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu			
210 215 220			
tta aat ggt aaa ctt gac ggt gct gca caa cgt gtt cct gtt cca act	720		
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr			
225 230 235 240			
gga tca gta act gaa tta gta gca gtt ctt gaa aaa gat act tca gta	768		
Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Asp Thr Ser Val			
245 250 255			
gaa gaa atc aat gca gct atg aaa gca gca gct aac gat tca tac ggt	816		
Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly			
260 265 270			
tac act gaa gat gct atc gta tca tca gat atc gta ggt att tct tac	864		
Tyr Thr Glu Asp Ala Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr			
275 280 285			
ggt tca tta ttt gat gct act caa act aaa gta caa act gtt gat gga	912		
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly			
290 295 300			
aat caa ttg gtt aaa gtt gtt tca tgg tat gac aat gaa atg tct tac	960		
Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr			
305 310 315 320			
act gct caa ctt gtt cgt act ctt gag tac ttt gca aaa atc gct aaa	1008		
Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys			
325 330 335			
taa	1011		

<210> 12  
 <211> 336  
 <212> PRT  
 <213> Streptococcus iniae

<400> 12  
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                     20                    25                    30  
 Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp  
             35                    40                    45  
 Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly  
     50                    55                    60  
 Phe Glu Val Asn Gly Ser Phe Val Lys Val Ser Ala Glu Arg Glu Pro  
     65                    70                    75                    80  
 Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Asp Ile Val Leu Glu Ala  
                     85                    90                    95  
 Thr Gly Phe Phe Ala Ser Lys Ala Ala Ala Glu Gln His Ile His Ala  
             100                    105                    110  
 Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val  
             115                    120                    125  
 Lys Thr Val Val Tyr Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu  
     130                    135                    140  
 Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met  
     145                    150                    155                    160  
 Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr  
             165                    170                    175  
 Thr Ile His Gly Tyr Thr Gly Asp Gln Met Val Leu Asp Gly Pro His  
             180                    185                    190  
 Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Ala Ala Asn Ile Val  
             195                    200                    205  
 Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu  
     210                    215                    220  
 Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr  
     225                    230                    235                    240  
 Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Asp Thr Ser Val  
             245                    250                    255



Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly  
260 265 270

Tyr Thr Glu Asp Ala Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr  
275 280 285

Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly  
290 295 300

Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr  
305 310 315 320

Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys  
325 330 335

<210> 13  
<211> 961  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: SpyGapC

<400> 13  
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tccaaatatg cttgcacact tgttgaaata cgatacaact caaggacgtt ttgatggaac 120  
agttgaagtt aaagaagggt gatttgaagt aaacggaaac ttcatacaag tttctgctga 180  
acgtgatcca gaaaacatcg actgggcaac tgatgggggtt gaaatcggtc tggaagcaac 240  
tggtttcttt gctaaaaaag aagcagctga aaaacactta catgctaacg gtgctaaaaa 300  
agttgttatc acagctcctg gtggaaacga tgtaaaaaca gttgttttca aactaacca 360  
cgacattctt gacggtactg aaacagttat ctcaggtgct tcatgtacta caaactgttt 420  
agtccttatg gctaaagtc ttcacgatgc attcgggtatc caaaaagggtc ttatgactac 480  
aatccacgct tatactgggtg accaaatgat ccttgacgga ccacaccgtg gtggtgacct 540  
tcgtcgtgca cgcgctgggtg ctgcaaacad tgttcctaac tcaactgggtg ctgctaaagc 600  
tatcgggtctt gttatcccag aacttaacgg taaacttgat ggtgctgcac aacgtgttcc 660  
tgttccaact ggatcagtaa ctgagttggt tgtaactctt gacaaaaacg tttctgttga 720  
cgaaatcaac tctgctatga aagctgcttc aaacgacagc ttcgggttaca ctgaagatcc 780  
aattgtttct tcagatatcg taggcgtatc atacggttca ttgtttgacg caactcaaac 840  
taaagtaatg gaagttgacg gatcacaatt gggttaaagt gtatcatggt atgacaacga 900  
aatgtcttac actgctcaac ttgtacgtac tcttgagtat ttcgcaaaaa ttgctaaata 960  
a 961

<210> 14  
<211> 335  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: SpyGapC  
protein

<400> 14  
Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu

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Ala	Phe	Arg	Arg	Ile	Gln	Asn	Ile	Glu	Gly	Val	Glu	Val	Thr	Arg	Ile
		20						25					30		
Asn	Asp	Leu	Thr	Asp	Pro	Asn	Met	Leu	Ala	His	Leu	Leu	Lys	Tyr	Asp
		35					40					45			
Thr	Thr	Gln	Gly	Arg	Phe	Asp	Gly	Thr	Val	Glu	Val	Lys	Glu	Gly	Gly
	50					55					60				
Phe	Glu	Val	Asn	Gly	Asn	Phe	Ile	Lys	Val	Ser	Ala	Glu	Arg	Asp	Pro
65					70					75					80
Glu	Ile	Asp	Trp	Ala	Thr	Asp	Gly	Val	Glu	Ile	Val	Leu	Glu	Ala	Thr
				85					90					95	
Ser	Phe	Phe	Ala	Lys	Lys	Glu	Ala	Ala	Glu	Lys	His	Leu	His	Ala	Asn
			100					105					110		
Gly	Ala	Lys	Lys	Val	Val	Ile	Thr	Ala	Pro	Gly	Gly	Asn	Asp	Val	Lys
	115						120					125			
Thr	Val	Val	Phe	Asn	Thr	Asn	His	Asp	Ile	Leu	Asp	Gly	Thr	Glu	Thr
	130					135					140				
Val	Ile	Ser	Gly	Ala	Ser	Cys	Thr	Thr	Asn	Cys	Leu	Ala	Pro	Met	Ala
145					150					155					160
Lys	Ala	Leu	His	Asp	Ala	Phe	Gly	Ile	Gln	Lys	Gly	Leu	Met	Thr	Thr
				165					170					175	
Ile	His	Ala	Tyr	Thr	Gly	Asp	Gln	Met	Ile	Leu	Asp	Gly	Pro	His	Arg
		180						185					190		
Gly	Gly	Asp	Leu	Arg	Arg	Ala	Arg	Ala	Gly	Ala	Ala	Asn	Ile	Val	Pro
	195						200					205			
Asn	Ser	Thr	Gly	Ala	Ala	Lys	Ala	Ile	Gly	Leu	Val	Ile	Pro	Glu	Leu
	210					215					220				
Asn	Gly	Lys	Leu	Asp	Gly	Ala	Ala	Gln	Arg	Val	Pro	Val	Pro	Thr	Gly
225					230					235					240
Ser	Val	Thr	Glu	Leu	Val	Val	Thr	Leu	Asp	Lys	Asn	Val	Ser	Val	Asp
			245						250					255	
Glu	Ile	Asn	Ser	Ala	Met	Lys	Ala	Ala	Ser	Asn	Asp	Ser	Phe	Gly	Tyr
		260						265					270		
Thr	Glu	Asp	Pro	Ile	Val	Ser	Ser	Asp	Ile	Val	Gly	Val	Ser	Tyr	Gly
	275						280					285			
Ser	Leu	Phe	Asp	Ala	Thr	Gln	Thr	Lys	Val	Met	Glu	Val	Asp	Gly	Ser

290 295 300

Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr Thr  
 305 310 315 320

Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys  
 325 330 335

<210> 15  
 <211> 1010  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: SeqGapC

<400> 15  
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 cttgcacact tgttgaaata cgatacaact caaggacggt ttgacggaac tggtgaagtt 180  
 aaagaagggtg gatttgaagt aaacggaaac ttcataaaag tttctgctga acgtgatcca 240  
 gaaaacatcg actgggcaac tgacggtggt gaaatcggtc tggaagcaac tggtttcttt 300  
 gctaaaaaag aagctgctga aaaaccctta catgctaacg gtgctaaaaa agttgttatc 360  
 acagctcctg gtggaaacga cgttaaacag ttgttttcaa cactaaccac gacattcttg 420  
 acggtactga aacagttatc tcaggtgctt catgtactac aaactgttta gctcctatgg 480  
 ctaaagctct tcacgatgca tttggtatcc aaaaagggtc tatgactaca atccacgctt 540  
 atactggtga ccaaattgatc gttgatggac accgtgggtg tggatgatctt cgtcgtgctc 600  
 gtgctggtgc tgcaaacatt gttcctaact caactgggtg tcgtaaagct atcgggtcttg 660  
 ttatcccaga attgaacggt aaacttgatg gtgctgcaca acgtgttcct gttccaactg 720  
 gatcagtaac tgagttggtt gtaactcttg acaaaaacgt ttctgttgac gaaatcaacg 780  
 ctgctatgaa agctgcttca aacgacagct tcggttacac tgaagatcca attgtttctt 840  
 cagatatcgt aggcgtatca tacggttcat tgtttgacgc aactcaaact aaagttatgg 900  
 aagttgatgg atcacaattg gttaaagttg tatcatggta tgacaacgaa atgtcttaca 960  
 ctgctcaact tgttcgtaca cttgagtatt ttgcaaaaat cgctaaataa 1010

<210> 16  
 <211> 336  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: SeqGapC  
 protein

<400> 16  
 Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu  
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 Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile  
 20 25 30  
 Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp  
 35 40 45

Thr	Thr	Gln	Gly	Arg	Phe	Asp	Gly	Thr	Val	Glu	Val	Lys	Glu	Gly	Gly		
	50					55					60						
Phe	Glu	Val	Asn	Gly	Asn	Phe	Ile	Lys	Val	Ser	Ala	Glu	Arg	Asp	Pro		
65					70					75					80		
Glu	Asn	Ile	Asp	Trp	Ala	Thr	Asp	Gly	Val	Glu	Ile	Val	Leu	Glu	Ala		
				85					90					95			
Thr	Ser	Phe	Phe	Ala	Lys	Lys	Glu	Ala	Ala	Glu	Lys	Pro	Leu	His	Ala		
				100				105					110				
Asn	Gly	Ala	Lys	Lys	Val	Val	Ile	Thr	Ala	Pro	Gly	Gly	Asn	Asp	Val		
		115					120					125					
Lys	Gln	Leu	Phe	Ser	Thr	Leu	Thr	Thr	Ser	Ile	Leu	Asp	Gly	Thr	Glu		
	130					135					140						
Thr	Val	Ile	Ser	Gly	Ala	Ser	Cys	Thr	Thr	Asn	Cys	Leu	Ala	Pro	Met		
145					150					155					160		
Ala	Lys	Ala	Leu	His	Asp	Ala	Phe	Gly	Ile	Gln	Lys	Gly	Leu	Met	Thr		
				165					170					175			
Thr	Ile	His	Ala	Tyr	Thr	Gly	Asp	Gln	Met	Ile	Val	Asp	Gly	His	Arg		
			180					185					190				
Gly	Gly	Gly	Asp	Leu	Arg	Arg	Ala	Arg	Ala	Gly	Ala	Ala	Asn	Ile	Val		
		195					200					205					
Pro	Asn	Ser	Thr	Gly	Ala	Arg	Lys	Ala	Ile	Gly	Leu	Val	Ile	Pro	Glu		
	210					215					220						
Leu	Asn	Gly	Lys	Leu	Asp	Gly	Ala	Ala	Gln	Arg	Val	Pro	Val	Pro	Thr		
225					230					235					240		
Gly	Ser	Val	Thr	Glu	Leu	Val	Val	Thr	Leu	Asp	Lys	Asn	Val	Ser	Val		
				245					250					255			
Asp	Glu	Ile	Asn	Ala	Ala	Met	Lys	Ala	Ala	Ser	Asn	Asp	Ser	Phe	Gly		
			260					265					270				
Tyr	Thr	Glu	Asp	Pro	Ile	Val	Ser	Ser	Asp	Ile	Val	Gly	Val	Ser	Tyr		
		275					280					285					
Gly	Ser	Leu	Phe	Asp	Ala	Thr	Gln	Thr	Lys	Val	Met	Glu	Val	Asp	Gly		
		290				295					300						
Ser	Gln	Leu	Val	Lys	Val	Val	Ser	Trp	Tyr	Asp	Asn	Glu	Met	Ser	Tyr		
305					310					315					320		
Thr	Ala	Gln	Leu	Val	Arg	Thr	Leu	Glu	Tyr	Phe	Ala	Lys	Ile	Ala	Lys		
				325					330					335			

<210> 17  
 <211> 933  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: BovGapC

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 Tyr Met Phe Gln Tyr Asp Ser Thr His Gly Lys Phe Asn Gly Thr Val  
 35 40 45  
 Lys Ala Glu Asn Gly Lys Leu Val Ile Asn Gly Lys Ala Ile Thr Ile  
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 Phe Gln Glu Arg Asp Pro Ala Asn Ile Lys Trp Gly Asp Ala Gly Ala  
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Glu	Tyr	Val	Val	Glu	Ser	Thr	Ser	Val	Phe	Thr	Thr	Met	Glu	Lys	Ala	85	90	95	
Gly	Ala	His	Leu	Lys	Gly	Gly	Ala	Lys	Arg	Val	Ile	Ile	Ser	Ala	Pro	100	105	110	
Ser	Ala	Asp	Ala	Pro	Met	Phe	Val	Met	Gly	Val	Asn	His	Glu	Lys	Tyr	115	120	125	
Asn	Asn	Thr	Leu	Lys	Ile	Val	Ser	Asn	Ala	Ser	Cys	Thr	Thr	Asn	Cys	130	135	140	
Leu	Ala	Pro	Leu	Ala	Lys	Val	Ile	His	Asp	His	Phe	Gly	Ile	Val	Glu	145	150	155	160
Gly	Leu	Met	Thr	Thr	Val	His	Ala	Ile	Thr	Ala	Thr	Gln	Lys	Thr	Val	165	170	175	
Asp	Gly	Pro	Ser	Gly	Lys	Leu	Trp	Arg	Asp	Gly	Arg	Gly	Ala	Ala	Gln	180	185	190	
Asn	Ile	Ile	Pro	Ala	Ser	Thr	Gly	Ala	Ala	Lys	Ala	Val	Gly	Lys	Val	195	200	205	
Ile	Pro	Glu	Leu	Asn	Gly	Lys	Leu	Thr	Gly	Met	Ala	Phe	Arg	Val	Pro	210	215	220	
Thr	Pro	Asn	Val	Ser	Val	Val	Asp	Leu	Thr	Cys	Arg	Leu	Glu	Lys	Pro	225	230	235	240
Ala	Lys	Tyr	Asp	Glu	Ile	Lys	Lys	Val	Val	Lys	Gln	Ala	Ser	Glu	Gly	245	250	255	
Pro	Leu	Lys	Gly	Ile	Leu	Gly	Tyr	Thr	Glu	Asp	Gln	Val	Val	Ser	Cys	260	265	270	
Asp	Phe	Asn	Ser	Asp	Thr	His	Ser	Ser	Thr	Phe	Asp	Ala	Gly	Ala	Gly	275	280	285	
Ile	Ala	Leu	Asn	Asp	His	Phe	Val	Lys	Leu	Ile	Ser	Trp	Tyr	Asp	Asn	290	295	300	
Glu	Phe	Gly	Tyr	Ser	Lys	Gln										305	310		